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We claim:

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1. A method for detecting predisposition to high altitude pulmonary edema (HAPE), said method comprising the steps of:

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(a) selecting study subjects by monitoring high altitude pulmonary edema associated symptoms,

(b) extracting genomic DNA from leukocytes by conventional methods from the study subjects,

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(c) amplifying Intron 7 of the human iNOS gene of SEQ ID No.1 by designing and synthesizing Forward and Reverse oligonucleotide primers of SEQ ID No. 2 and SEQ ID No. 3, respectively,

(d) identifying computationally the Novel Single Nucleotide Polymorphism (SNP) by comparing with the already existing sequence of human iNOS gene,

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(e) screening the high altitude native population (HA natives), low lander natives (HAPE controls) and low lander HAPE patients for the novel single nucleotide polymorphism, using above said primers of SEQ ID No. 2 (Forward Primer) and SEQ ID 3 (Reverse Primer),

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(f) computing the frequencies of AA, AG and GG genotypes in the populations of step (d) for establishing the association of the genotypes with high altitude pulmonary edema, and

(g) predicting and statistically analyzing differences in the distribution of the allelic variants (AA, AG and GG genotypes) in the populations and wherein GG genotype at 19480 position are at low risk to high altitude pulmonary edema and AA genotype at 19480 position are at high risk to of the high altitude pulmonary edema.

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2. A method as claimed in claim 1 wherein, the oligonucleotide primers capable for amplification of Intron 7 of human iNOS gene are selected from group

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7. The nucleic acid vectors containing the allelic variants of the iNOS gene.